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OM nucleic - nucleic search, using sw model

Run on: December 23, 2005, 20:51:02 ; Search time 290 Seconds
(without alignments)
8808.124 Million cell updates/sec

Title: US-09-869-079D-2
Perfect score: 1437
Sequence: 1 atgagcgatgttaccattgt.....actctgcaagtgagacgagaa 1437

Scoring table: OLIGO NUC
Gapop_60.0 , Gapext 60.0

Searched: 1303057 seqs, 888780828 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA.*
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5: /cgn2_6/ptodata/1/ina/H COMB.seq.*
6: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
7: /cgn2_6/ptodata/1/ina/PP COMB.seq.*
8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1437	100.0	1547	3	US-09-851-670-1
2	1354	94.2	1570	3	US-09-526-043-1
3	743	51.7	2410	3	US-09-771-161A-66
4	562	39.1	968	3	US-09-771-161A-65
5	403	28.0	403	3	US-09-474-922A-1
6	285	19.8	387	3	US-09-474-922A-2
7	197	13.7	265	3	US-09-513-999C-2948
8	172	12.0	765	3	US-09-771-161A-64
9	104	7.2	106	3	US-09-513-999C-23043
10	90	6.3	94	3	US-09-513-999C-16008
11	74	5.1	74	3	US-09-526-043-5
12	29	2.0	29	3	US-09-474-922A-3
13	27	1.9	27	3	US-09-474-922A-4
14	25	1.9	27	3	US-09-474-922A-5
15	25	1.7	25	3	US-09-474-922A-6
16	25	1.7	25	3	US-09-474-922A-7
17	25	1.7	25	3	US-09-851-670-6
18	25	1.7	25	3	US-09-851-670-12
19	24	1.7	24	3	US-09-474-922A-8
20	24	1.7	24	3	US-09-851-670-2
21	24	1.7	194	3	US-09-513-999C-35160
22	23	1.6	1254	3	US-09-580-740-3
23	23	1.6	1599	3	US-09-256-465-1
24	23	1.6	1599	3	US-09-167-322-3

25	23	1.6	1599	3	US-09-023-655-1004	Sequence 1004, Ap
26	23	1.6	2181	3	US-09-417-197-70	Sequence 70, Appl
27	23	1.6	2184	3	US-09-417-197-138	Sequence 138, Ap
28	23	1.6	2239	3	US-09-949-016-1676	Sequence 1676, Ap
29	23	1.6	2599	9	5266464-1	Patent No. 5266464
30	23	1.6	2610	2	US-09-212-771-1	Sequence 1, Appli
31	23	1.6	2610	3	US-09-091-058-1	Sequence 1, Appli
32	23	1.6	2610	3	US-09-023-655-1206	Sequence 1206, Ap
33	23	1.6	2610	3	US-09-590-740-1	Sequence 1, Appli
34	23	1.6	3321	3	US-09-023-655-1361	Sequence 1361, Ap
35	23	1.6	236474	3	US-09-949-016-13418	Sequence 13418, A
36	22	1.5	22	3	US-09-526-043-4	Sequence 4, Appli
37	22	1.5	26	3	US-09-851-670-18	Sequence 18, Appli
38	22	1.5	90	3	US-09-526-043-7	Sequence 7, Appli
39	21	1.5	23	3	US-09-851-670-15	Sequence 15, Appli
40	21	1.5	36	3	US-10-473-785-8	Sequence 8, Appli
41	21	1.5	36	3	US-10-473-763-8	Sequence 8, Appli
42	21	1.5	78491	3	US-09-949-016-15132	Sequence 15132, A
43	20	1.4	25	3	US-09-851-670-19	Sequence 19, Appli
44	20	1.4	48	3	US-10-473-785-10	Sequence 10, Appli
45	20	1.4	48	3	US-10-473-763-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1
US-09-851-670-1
; Sequence 1, Application US/09851670
; Patent No. 6809194
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; TITLE OF INVENTION: AKT3 INHIBITORS
; FILE REFERENCE: PP-01699.002/200130.520
; CURRENT APPLICATION NUMBER: US/09/851,670
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-851-670-1

Query Match 100.0%; Score 1437; DB 3; Length 1547;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGAGCGATGTTACCAATGTGAAAGAGGTTGGGTTTCAGAAAGGGGAGAGATATATAAAA	60
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Qy	61	AACAGGAGGCAAGATACCTCTTTTGAACACAGATGGCTCATTATAGATATAAGAG	120
Db	71	AACAGGAGGCAAGATACCTCTTTTGAACACAGATGGCTCATTATAGATATAAGAG	130
Qy	121	AAACCTCAAGATGTGGATTACCTTATCCCTCAACAACCTTTTCAGTGGCAAAATGCCAG	180
Db	131	AAACCTCAAGATGTGGATTACCTTATCCCTCAACAACCTTTTCAGTGGCAAAATGCCAG	190
Qy	181	TTAATGAAACAGAACGACAAAGCCAAACACATTTTATATAGATGTCTCCAGTGACT	240
Db	251	ACTGTTATAGAGAAACATTTTCATGTAGATACCTCCAGAGAAAGGAGAGATGGACAGAA	310
Qy	301	GCTATCCAGGCTGTAGCAGACACTGTCAGAGGCAAGAGGAGAGAGAAATGAATTGTAGT	360
Db	311	GCTATCCAGGCTGTAGCAGACACTGTCAGAGGCAAGAGGAGAGAGAAATGAATTGTAGT	370

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QY 481 AAAGTTATTTTGGTTCGAGAGAGGCAAGTGGAAATACTATGCTATGAAGATTTCTGAAG 540
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Db |||||
QY 551 AAAGAAGTCATTTATGCGAAAGATGAAGTGGCACACACTCTTAACGTGAAGAGAGATATTA 610
Db |||||
QY 601 AAGAACACTAGACATCCCTTTTAAACATCTTTGAAATATTTCTTCAGACAAAGACCGT 660
Db |||||
QY 611 AAGAACACTAGACATCCCTTTTAAACATCTTTGAAATATTTCTTCAGACAAAGACCGT 670
Db |||||
QY 661 TTGTGTTTTGTGATGGAATATGTTAATGGGGGCGAGCTGTTTTCCATTTGTCGAGAGAG 720
Db |||||
QY 671 TTGTGTTTTGTGATGGAATATGTTAATGGGGGCGAGCTGTTTTCCATTTGTCGAGAGAG 730
Db |||||
QY 721 CGGGTGTTCTCTGAGGACCGCACACGTTTTCTATGTTGTCGAGAAATGTCCTGCTTGGAC 780
Db |||||
QY 731 CGGGTGTTCTCTGAGGACCGCACACGTTTTCTATGTTGTCGAGAAATGTCCTGCTTGGAC 790
Db |||||
QY 781 TATCTACATTCGCGAAAGATGTTGACCGTGATCTCAAGTGGAGAACTAATGCTGGAC 840
Db |||||
QY 791 TATCTACATTCGCGAAAGATGTTGACCGTGATCTCAAGTGGAGAACTAATGCTGGAC 850
Db |||||
QY 841 AAAGATGGCCACATAAAAATTACAGATTTTGACATTTGCAAAAGAGGGATCACAGATGCA 900
Db |||||
QY 851 AAAGATGGCCACATAAAAATTACAGATTTTGACATTTGCAAAAGAGGGATCACAGATGCA 910
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QY 901 GCCACATGAAGACATTTCTGGGCACTCAGAAATATCTGGGCAACGAGGTGTTAGAAGAT 960
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QY 911 GCCACATGAAGACATTTCTGGGCACTCAGAAATATCTGGGCAACGAGGTGTTAGAAGAT 970
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QY 961 AATGACTATGGCGGAGCAGTACACTGGTGGGCGCTAGGGGTTGTCATGTATCAATATGATG 1020
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QY 1021 TGTGGAGGTTTACCTTTCTTCAACACGAGCACATGAGAAACTTTTGAATTAATTAATG 1080
Db |||||
QY 1031 TGTGGAGGTTTACCTTTCTTCAACACGAGCACATGAGAAACTTTTGAATTAATTAATG 1090
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QY 1081 GAAGACATTTAAATTTCTCGAACAATCTCTTTCAGATGCAAAATCATTTGCTTTCAGGGCTC 1140
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QY 1091 GAAGACATTTAAATTTCTCGAACAATCTCTTTCAGATGCAAAATCATTTGCTTTCAGGGCTC 1150
Db |||||
QY 1141 TTGATAAAGGATCCAAATAAAACGCTTGGTGGAGGACGAGATGATGCAAAAGAAATATG 1200
Db |||||
QY 1151 TTGATAAAGGATCCAAATAAAACGCTTGGTGGAGGACGAGATGATGCAAAAGAAATATG 1210
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QY 1201 AGACACAGTTTCTTCTCTGGAGTAAACTGGCAGAGATGTATATGATAAAAGCTTGTACCT 1260
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QY 1211 AGACACAGTTTCTTCTCTGGAGTAAACTGGCAGAGATGTATATGATAAAAGCTTGTACCT 1270
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QY 1261 CCTTTTAAACCTCAAGTAAACATCTGAGACAGATACCTAGATATTTTGTATGAAGAAATTTACA 1320
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QY 1271 CCTTTTAAACCTCAAGTAAACATCTGAGACAGATACCTAGATATTTTGTATGAAGAAATTTACA 1330
Db |||||
QY 1321 GCTCAGACTATTACAAATACACCACTGGAATAATATGATGAGGATGGTATGACCTGCATG 1380
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QY 1331 GCTCAGACTATTACAAATACACCACTGGAATAATATGATGAGGATGGTATGACCTGCATG 1390
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QY 1381 GACAAATGAGAGCGGCGCGCATTTCCCTCAATTTTCTTACTCTGCAAGTGGACGAGAA 1437
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QY 1391 GACAAATGAGAGCGGCGCGCATTTCCCTCAATTTTCTTACTCTGCAAGTGGACGAGAA 1447
Db |||||
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RESULT 2
US-09-526-043-1
; Sequence 1, Application US/09526043
; Patent No. 6881555
; GENERAL INFORMATION:
; APPLICANT: Guo, Kun
; APPLICANT: Pagnoni, Marco
; APPLICANT: Clark, Kenneth
; APPLICANT: Ivashchenko, Yuri
; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
; FILE REFERENCE: A3278A-US
; CURRENT APPLICATION NUMBER: US/09/526,043
; CURRENT FILING DATE: 2000-03-14
; EARLIER APPLICATION NUMBER: 60/125,108
; EARLIER FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1570
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (126)..(1523)
US-09-526-043-1
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Query Match          94.2%; Score 1354; DB 3; Length 1570;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61  AACTGGAGGCCAAGATACCTTCTTTTGAAGACAGATGCTCATTCATAGGATATAAAGAG 120
Db  |||||
QY 186 AACTGGAGGCCAAGATACCTTCTTTTGAAGACAGATGCTCATTCATAGGATATAAAGAG 245
Db  |||||
QY 121 AAACCTCAAGATGTGGATTTACCTTTATCCCTCAACAACTTTTTCAGTGGCAAAATGCCAG 180
Db  |||||
QY 246 AAACCTCAAGATGTGGATTTACCTTTATCCCTCAACAACTTTTTCAGTGGCAAAATGCCAG 305
Db  |||||
QY 181 TTAATGAAAAACAGAACGACCAAGCCAAACACATTTTAAATCAGATGTCTCCAGTGGACT 240
Db  |||||
QY 306 TTAATGAAAAACAGAACGACCAAGCCAAACACATTTTAAATCAGATGTCTCCAGTGGACT 365
Db  |||||
QY 241 ACTGTTATAGAGACACATTTTCATGTAGATACTCCAGAGGAAGGAAATGGACAGAA 300
Db  |||||
QY 366 ACTGTTATAGAGACACATTTTCATGTAGATACTCCAGAGGAAGGAAATGGACAGAA 425
Db  |||||
QY 301 GCTATCCAGGCTGTAGCAGACAGACTGCGAGAGGCAAGAGAGGAGAGAAATGAATTTGTAGT 360
Db  |||||
QY 426 GCTATCCAGGCTGTAGCAGACAGACTGCGAGGCGNAGAGAGGAGAGAAATGAATTTGTAGT 485
Db  |||||
QY 361 CCAACTTCACAAATTTGATTAATATAGGAGAGGAGAGATGGATGCTCTACAAACCCATCAT 420
Db  |||||
QY 486 CCAACTTCACAAATTTGATTAATATAGGAGAGGAGAGATGGATGCTCTACAAACCCATCAT 545
Db  |||||
QY 421 AAAAGAAAGACAAATGAATGATTTTGAACCTACTAGGTAAAGGCACTTTTGGG 480
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QY 546 AAAAGAAAGACAAATGAATGATTTTGAACCTACTAGGTAAAGGCACTTTTGGG 605
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QY 606 AAAGTTATTTTGGTTCGAGAGAGGCAAGTGGAAAAATACTATGCTATGAAGATTTCTGAAG 665
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QY 541 AAAGAAGTCATTTATGCGAAAGGATGAAGTGGCACACACTCTTAACCTGAAAGCAGAGATATTA 600
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QY 666 AAAGAAGTCATTTATGCGAAAGGATGAAGTGGCACACACTCTTAACCTGAAAGCAGAGATATTA 725
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QY 601 AAGAACACTAGACATCCCTTTTAAACATCTTTTAACTCTTGAATATTTCTTCCACACAAAGACCGT 660
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QY 726 AAGAACACTAGACATCCCTTTTAAACATCTTTTGAATATTTCTTCCACACAAAGACCGT 785
Db  |||||
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661 TTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTCATTTGTCGAGAGAG 720
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Db CGGGTGTCTCTGAGGACCGCACAGTTTCTATGTCGAGAAATGCTCTGCTTGGAC 905
781 TATCTACATTCGGGAAAGATTGTGTACCGTGATCTCAAGTTGGAGAAATCTAATGCTGGAC 840
Db TATCTACATTCGGGAAAGATTGTGTACCGTGATCTCAAGTTGGAGAAATCTAATGCTGGAC 965
841 AAAGATGGCCACATAAATAATACAGATTTTGGCTTTGCAAGAGGGATCACAGATGCA 900
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961 AATGACTATGGCGGACGAGTAGACTGTGGGGCTAGGGGTTGTCTATGTATGAAATGATG 1020
Db AATGACTATGGCGGACGAGTAGACTGTGGGGCTAGGGGTTGTCTATGTATGAAATGATG 1145
1021 TGTGGAGGTTTACCTTTCTACACAGGACCATGAGAAATCTTTTGAATTAATTAATG 1080
Db TGTGGAGGTTTACCTTTCTACACAGGACCATGAGAAATCTTTTGAATTAATTAATG 1205
1081 GAAGACATTAATTTCTCGAACACTCTTTCAGATGCAAAATCATTTCTCAGGGCTC 1140
Db GAAGACATTAATTTCTCGAACACTCTTTCAGATGCAAAATCATTTCTCAGGGCTC 1265
1141 TTGATAAAGGATCCAAATAACCCCTTGTGGAGGACCATGATGCAAAAGAAATATG 1200
Db TTGATAAAGGATCCAAATAAACCCTTGTGGAGGACCATGATGCAAAAGAAATATG 1325
1201 AGACAGATTTCTCTCTGAGTAAACTGGCAAGATGATATGATATAAAGCTTTGACCT 1260
Db AGACAGATTTCTCTCTGAGTAAACTGGCAAGATGATATGATATAAAGCTTTGACCT 1385
1261 CCTTTAAACCTCAAGTAACTCTGACAGACATAGATATTTGATGAAGATTTACA 1320
Db CCTTTAAACCTCAAGTAACTCTGACAGACATAGATATTTGATGAAGATTTACA 1445
1321 GCTCAGACTATTCAATAACACACACCTGAAAAAT 1354
Db GCTCAGACTATTCAATAACACACCTGAAAAAT 1479

RESULT 3

US-09-771-161A-66
; Sequence 66, Application US/09771161A
; Patent No. 6936450
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR FILING DATE: 09/724,676
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 66
; LENGTH: 2410
; ORGANISM: Homo sapiens
US-09-771-161A-66

Query Match 51.7%; Score 743; DB 3; Length 2410;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 743; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 695 AGCTGTTTTTCATTTGTCGAGAGAGCGGGTGTCTCTGAGGACCGCACACGTTTCTATG 754
Db 312 AGCTGTTTTTCATTTGTCGAGAGAGCGGGTGTCTCTGAGGACCGCACACGTTTCTATG 371
755 GTGCAAGAAATGTCTGCTGCTTGGACTATCTATACATTCGGAAGAAATGTGTACCGTGATC 814
Db 372 GTGCAAGAAATGTCTGCTGCTTGGACTATCTATACATTCGGAAGAAATGTGTACCGTGATC 431
815 TCAAGTTCGGAAGAAATCTAATGCTGGCAAGAAATGCGCACATAAATAATACAGATTTTGGAC 874
Db 432 TCAAGTTCGGAAGAAATCTAATGCTGGCAAGAAATGCGCACATAAATAATACAGATTTTGGAC 491
875 TTTGCAAGAAAGGGATCACAGATGCGACCAACCATGAAGACATTTCTGTGSCACTCCAGAAAT 934
Db 492 TTTGCAAGAAAGGGATCACAGATGCGACCAACCATGAAGACATTTCTGTGSCACTCCAGAAAT 551
935 ATCTGGCACAGAGGTGTAGAAATGATCTATGGCGGAGCAGTAGACTGGTGGGGCC 994
Db 552 ATCTGGCACAGAGGTGTAGAAATGATCTATGGCGGAGCAGTAGACTGGTGGGGCC 611
995 TAGGGGTTGTCTATGTAATGATGTGTGGGAGGTACCTTTCTACACACGAGGACCATG 1054
Db 612 TAGGGGTTGTCTATGTAATGATGTGTGGGAGGTACCTTTCTACACACGAGGACCATG 671
1055 AGAAACTTTTTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1114
Db 672 AGAAACTTTTTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 731
1115 ATGCAAAATCATTTGCTTTCAGGGCTCTTGATAAAGATCCAAATAAAGCTTTGTTGGAG 1174
Db 732 ATGCAAAATCATTTGCTTTCAGGGCTCTTGATAAAGATCCAAATAAAGCTTTGTTGGAG 791
1175 GACCAGATGATGCAAAAGAAATTAAGACACAGATTTCTCTGAGTAAAGCTGGCAAG 1234
Db 792 GACCAGATGATGCAAAAGAAATTAAGACACAGATTTCTCTGAGTAAAGCTGGCAAG 851
1235 ATGTATATGATATAAAGCTTTGACCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATA 1294
Db 852 ATGTATATGATATAAAGCTTTGACCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATA 911
1295 CTAGATATTTTGTATGAAGAAATTTACAGCTCAGACTATTACAAATAACCAACCTGAAAAAT 1354
Db 912 CTAGATATTTTGTATGAAGAAATTTACAGCTCAGACTATTACAAATAACCAACCTGAAAAAT 971
1355 ATGATGAGGATGTTATGGACTGATGAGCAATGAGAGGGCGGCATTTCCCTCAATTTT 1414
Db 972 ATGATGAGGATGTTATGGACTGATGAGCAATGAGAGGGCGGCATTTCCCTCAATTTT 1031
QY 1415 CCTACTCTGCAAGTGGACGAGAA 1437
Db 1032 CCTACTCTGCAAGTGGACGAGAA 1054

RESULT 4

US-09-771-161A-65
; Sequence 65, Application US/09771161A
; Patent No. 6936450
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR FILING DATE: 09/724,676
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619

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; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 65
; LENGTH: 968
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: -
; LOCATION: (1)..(968)
; OTHER INFORMATION: "n" can be any nucleotide 'a', 'c', 'g' or 't'
US-09-771-161A-65

Query Match      39.1%; Score 562; DB 3; Length 968;
Best Local Similarity 100.0%; Pred. No. 4.8e-273;
Matches 562; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGCGATGTACCAATTTGGAAGAGGTTGGGTTTCAGAGAGGGGAGAAATATATAAA 60
Db 154 ATGAGCGATGTACCAATTTGGAAGAGGTTGGGTTTCAGAGAGGGGAGAAATATATAAA 213
QY 61 AACTGGAGGCCAAGATACCTCTTTGAAGACAGATGGCTCATTCATAGGATATAAAGAG 120
Db 214 AACTGGAGGCCAAGATACCTCTTTGAAGACAGATGGCTCATTCATAGGATATAAAGAG 273
QY 121 AAACCTCAAGATGTGGATTTACCTTATCCCTCAACAACTTTTCAGTGGCAAAATGCCAG 180
Db 274 AAACCTCAAGATGTGGATTTACCTTATCCCTCAACAACTTTTCAGTGGCAAAATGCCAG 333
QY 181 TTAATGMAACAGACGACCAAGCCAAAGCCAAACATTTATATCAGATGCTCCAGTGGACT 240
Db 334 TTAATGMAACAGACGACCAAGCCAAAGCCAAACATTTATATCAGATGCTCCAGTGGACT 393
QY 241 ACTGTTATAGAGAGAACATTTTCATGTAGATACCTCCAGAGGAAAGGGAAGATGGACAGAA 300
Db 394 ACTGTTATAGAGAGAACATTTTCATGTAGATACCTCCAGAGGAAAGGGAAGATGGACAGAA 453
QY 301 GCTATCCAGGCTGTAGCAGACAGACTGTCAGAGGCGCAAGAGAGAGAGAAATGTTAGT 360
Db 454 GCTATCCAGGCTGTAGCAGACAGACTGTCAGAGGCGCAAGAGAGAGAGAAATGTTAGT 513
QY 361 CCAACTTCACAAATTTGATATATAGAGAGGAGAGATGGATGCCCTTACACCCCATCAT 420
Db 514 CCAACTTCACAAATTTGATATATAGAGAGGAGAGATGGATGCCCTTACACCCCATCAT 573
QY 421 AAAAGAGACAAATGAATGATTTTGACTATTTGAACTACTAGGTAAAGGCACTTTTGGG 480
Db 574 AAAAGAGACAAATGAATGATTTTGACTATTTGAACTACTAGGTAAAGGCACTTTTGGG 633
QY 481 AAAGTTATTTTGGTTCGAGAGAGGCAAGTGGAAATATCTATGCTATGAAGATTCGAG 540
Db 634 AAAGTTATTTTGGTTCGAGAGAGGCAAGTGGAAATATCTATGCTATGAAGATTCGAG 693
QY 541 AAAGAGTCATTTATTCGAAGG 562
Db 694 AAAGAGTCATTTATTCGAAGG 715

RESULT 5
US-09-474-922A-1
; Sequence 1, Application US/09474922A
; Patent No. 6187586
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; APPLICANT: Richard A. Roth
; TITLE OF INVENTION: ANTISENSE MODULATION OF Akt-3 EXPRESSION
; FILE REFERENCE: RTS-0036
; CURRENT APPLICATION NUMBER: US/09/474,922A
; CURRENT FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 1
; LENGTH: 403
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-474-922A-2
; Sequence 2, Application US/09474922A
; Patent No. 6187586
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; APPLICANT: Richard A. Roth
; TITLE OF INVENTION: ANTISENSE MODULATION OF Akt-3 EXPRESSION
; FILE REFERENCE: RTS-0036
; CURRENT APPLICATION NUMBER: US/09/474,922A
; CURRENT FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 2
; LENGTH: 387
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-474-922A-2

Query Match      19.8%; Score 285; DB 3; Length 387;
Best Local Similarity 99.5%; Pred. No. 2.3e-133;
Matches 385; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 ATGACTATGGCCGAGCAGTAGACTGGTGGGCCCTTAGGGTTGTTCATGTATGAATGATGT 60
QY 1022 GTGGAGGTTACCTTTCTACACCCAGGACCAATGAGAACTTTTGAATTAATTAATG 1081
Db 61 GTGGAGGTTACCTTTCTACACCCAGGACCAATGAGAACTTTTGAATTAATTAATG 120
QY 1082 AAGACATTAATTTTCTCGAACACTCTTTCAGATGCAAAATCATTTGCTTTTCAGGGCTCT 1141
Db 121 AAGACATTAATTTTCTCGAACACTCTTTCAGATGCAAAATCATTTGCTTTTCAGGGCTCT 180
QY 1142 TGATAAAGGATCCAAATAAAGCGCTTGGTGAGGAGCCAGATGATGCAAAAGAAATTTATGA 1201
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Tue Dec 27 10:45:14 2005

US-09-474-922A-5
; Sequence 5, Application US/09474922A
; Patent No. 6187586
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; APPLICANT: Richard A. Roth
; TITLE OF INVENTION: ANTISENSE MODULATION OF Akt-3 EXPRESSION
; FILE REFERENCE: RTS-0036
; CURRENT APPLICATION NUMBER: US/09/474,922A
; CURRENT FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 5
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Probe
US-09-474-922A-5

Query Match 1.9%; Score 27; DB 3; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 305 TCACGGCTGTAGCAGACGACTGCAGA 331
Db 1 TCACGGCTGTAGCAGACGACTGCAGA 27

RESULT 15
US-09-474-922A-6
; Sequence 6, Application US/09474922A
; Patent No. 6187586
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; APPLICANT: Richard A. Roth
; TITLE OF INVENTION: ANTISENSE MODULATION OF Akt-3 EXPRESSION
; FILE REFERENCE: RTS-0036
; CURRENT APPLICATION NUMBER: US/09/474,922A
; CURRENT FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 6
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-09-474-922A-6

Query Match 1.7%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1135 GGGCTCTTGATAAAGGATCCAAATA 1159
Db 1 GGGCTCTTGATAAAGGATCCAAATA 25

Search completed: December 24, 2005, 00:01:46
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	451	94.2	1570	3	US-09-526-043-1
3	247	51.6	2410	3	US-09-771-161A-66
4	187	39.0	968	3	US-09-771-161A-65
5	134	28.0	403	3	US-09-474-922A-1
6	100	20.9	387	3	US-09-474-922A-2
7	61	12.7	1254	3	US-09-590-740-3
8	61	12.7	2181	3	US-09-417-197-70
9	61	12.7	2184	3	US-09-417-197-138

10	61	12.7	2610	2	US-09-212-771-1	Sequence 1, Appli
11	61	12.7	2610	3	US-09-091-058-1	Sequence 1, Appli
12	61	12.7	2610	3	US-09-023-653-1206	Sequence 1206, Ap
13	61	12.7	2610	3	US-09-590-740-1	Sequence 1, Appli
14	61	12.7	2626	3	US-09-590-740-5	Sequence 5, Appli
15	57	11.9	765	3	US-09-771-161A-64	Sequence 64, Appli
16	52	10.9	1599	3	US-09-256-465-1	Sequence 1, Appli
17	52	10.9	1599	3	US-09-167-322-3	Sequence 3, Appli
18	52	10.9	1599	3	US-09-023-653-1004	Sequence 1004, Ap
19	48	10.0	265	3	US-09-513-999C-2948	Sequence 2948, Ap
20	34	7.1	106	3	US-09-513-999C-23043	Sequence 23043, A
21	29	6.1	94	3	US-09-513-999C-16008	Sequence 16008, A
22	29	5.0	74	3	US-09-526-043-5	Sequence 5, Appli
23	21	4.4	1830	3	US-09-771-161A-41	Sequence 41, Appli
24	15	3.1	532	3	US-09-270-767-14090	Sequence 14090, A
25	14	2.9	1338	3	US-10-067-977-1	Sequence 1, Appli
26	14	2.9	2311	2	US-08-712-709-6	Sequence 6, Appli
27	14	2.9	2311	3	US-09-111-444-6	Sequence 6, Appli
28	14	2.9	2311	3	US-09-541-228-6	Sequence 6, Appli
29	14	2.9	2311	3	US-09-016-434-772	Sequence 772, App
30	14	2.9	2370	3	US-09-031-295-1	Sequence 1, Appli
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33	12	2.5	1413	3	US-09-248-796A-4379	Sequence 4379, Ap
34	11	2.3	186	3	US-09-270-767-13452	Sequence 13452, A
35	11	2.3	1503	3	US-09-797-039-3	Sequence 3, Appli
36	11	2.3	2297	3	US-09-797-039-1	Sequence 1, Appli
37	11	2.3	2747	3	US-09-620-312D-19	Sequence 19, Appli
38	11	2.3	2840	3	US-09-620-312D-20	Sequence 20, Appli
39	11	2.3	3124	3	US-09-734-030-1	Sequence 1, Appli
40	11	2.3	3124	3	US-10-153-921-1	Sequence 1, Appli
41	11	2.3	3124	3	US-10-669-689-1	Sequence 1, Appli
42	11	2.3	6034	3	US-09-949-016-711	Sequence 711, App
43	11	2.3	6046	3	US-09-949-016-5830	Sequence 5830, Ap
44	11	2.3	7220	3	US-09-949-016-3586	Sequence 3586, Ap
45	11	2.3	111235	3	US-09-949-016-15328	Sequence 15328, A

ALIGNMENTS

RESULT 1

US-09-851-670-1
; Sequence 1, Application US/09851670
; Patent No. 6809194
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; TITLE OF INVENTION: AKT3 INHIBITORS
; FILE REFERENCE: PP-01699.002/200130.520
; CURRENT APPLICATION NUMBER: US/09/851,670
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-851-670-1

Alignment Scores:
Pred. No.: 0 Length: 1547
Score: 479.00 Matches: 479
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-869-079D-3 (1-479) x US-09-851-670-1 (1-1547)

Qy 1 MetSerAspValThrIleValLysGluGlyTyrValGlnLysArgGlyGluTyrIleLys 20
Db 11 ATGAGCCATGTTACCATTTGAAAGAGAGTTGGGTTTCAGAGAGGGGAGATATATAAA 70

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QY 21 AsnTrpArgProArgTyrPheLeuLeuLysThrAspGlySerPheIleGlyTyrLysGlu 40
DB 71 AACTGAGGCCAAGATACTCTCTTTTGAAGACAGATGGCTCATTCATAGATATAAAGAG 130
QY 41 LysProGlnAspValAspLeuProTyrProLeuAsnAsnPheSerValAlaLysCysGln 60
DB 131 AAACCTCAAGATGTGGATTTACCTTATCCCTCAACAACCTTTTCAGTGGCAAAATGCCAG 190
QY 61 LeuMetLysThrGluArgProLysProAsnThrPheIleIleArgCysLeuGlnTrpThr 80
DB 191 TTAATGAACAACAGACGACCAAGCCAAACACATTTATTAATCAGATGTCTCCAGTGGACT 250
QY 81 ThrValIleGluArgThrPheHisValAspThrProGluGluArgGluTrpThrGlu 100
DB 251 ACTGTTATAGAGAACATTTCTATGTAGATACTCCAGAGGAAAGGGAATGGACAGAA 310
QY 101 AlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGluGluArgMetAsnCysSer 120
DB 311 GCTATCCAGGCTGTAGCAGACAGACTGCAGAGGCGAAGAGAGAGAGAAATGTTAGT 370
QY 121 ProThrSerGlnIleAspAsnIleGlyGluGluGluMetAspAlaSerThrThrHisHis 140
DB 371 CCAACTTCACAATTTGATTAATAGGAGAGGAGATGCGTCTCTACAACCCATCAT 430
QY 141 LysArgLysThrMetAsnAspPheAspTyrLeuLysLeuLeuGlyLysGlyThrPheGly 160
DB 431 AAAGAAAGACAAATGAATGATTTGACTATTGAAACTACTAGGTAAGGCACTTTTGGG 490
QY 161 LysValIleLeuValArgGluLysAlaSerGlyLysTyrTyrAlaMetLysIleLeuLys 180
DB 491 AAAGTTATTTTGGTTCGAGAGAGGCAAGTGGAAATACTATGCTATGAAGATTTCTGAAG 550
QY 181 LysGluValIleIleAlaLysAspGluValAlaHisThrLeuThrGluSerArgValLeu 200
DB 551 AAAGAAGTCATTTATGCAAGAGTGAAGTGGCACACACTCTAACTGAAAGCAGAGATTATA 610
QY 201 LysAsnThrArgHisProPheLeuThrSerLeuLysTyrSerPheGlnThrLysAspArg 220
DB 611 AAGAACACATAGACATCCCTTTTAAACATCCTTGAATAATTTCTTCAGACAAAGACCGT 670
QY 221 LeuCysPheValMetGluTyrValLysGlyGlyGluLeuPhePheHisLeuSerArgGlu 240
DB 671 TTGTGTTTGTGATGAAATATGTTAATGGGGCGAGCTGTTTTCATTTGTCGAGAGAG 730
QY 241 ArgValPheSerGluAspArgThrArgPheTyrGlyAlaGluIleValSerAlaLeuAsp 260
DB 731 CGGGTGTCTCTGAGGACCGCACACGTTTCTATGGTGCAGAAATTTGCTCTCGCTTGGAC 790
QY 261 TyrLeuHisSerGlyLysIleValTyrArgAspLeuLysLeuGluAsnLeuMetLeuAsp 280
DB 791 TATCTACATTCGGAAGATTTGTACCGTGATCTCAAGTTGGAGAATCTAATGCTGGAC 850
QY 281 LysAspGlyHisIleLysIleThrAspPheGlyLeuCysLysGluGlyIleThrAspAla 300
DB 851 AAAGATGGCCACATAAAAATTAACAGATTTTGACATTTGCAAAAGAGGGGATCACATGCA 910
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DB 1031 TGTGGAGGTTTACCTTTCTACAAACAGGACCATGAGAACTTTTGAATTAATAATAATG 1090
QY 361 GluAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeuSerGlyLeu 380
DB 1091 GAAGACATTAATTTCTCGNACACTCTCTTCAGATGCAAAATCATTTGCTTTCAGGGCTC 1150
QY 381 LeuIleLysAspProAsnLysArgLeuGlyGlyGlyProAspAspAlaLysGluIleMet 400
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DB 1211 AGACACAGTTCCTCTCTGGAGTAAACTGGCAAGATGTATATGATAAAAGCTTGTACCT 1270
QY 421 ProPheLysProGlnValThrSerGluThrAspThrArgTyrPheAspGluGluPheThr 440
DB 1271 CCTTTTAAACCTCAAGTAACATCTGAGACAGATACTAGATATTTTGTATGAAGAAATTACA 1330
QY 441 AlaGlnThrIleThrIleThrProProGluLysTyrAspGluAspGlyMetAspCysMet 460
DB 1331 GCTCAGACTATTACAATAAACACACCTGAAAAATATGATGAGGATGGTATGAGACTGCATG 1390
QY 461 AspAsnGluArgArgProHisPheProGlnPheSerTyrSerAlaSerGlyArgGlu 479
DB 1391 GACAAATGAGAGCGCGCCATTTCCCTCAATTTTCTACTCTGCAAGTGGACGAGAA 1447

RESULT 2
US-09-526-043-1
; Sequence 1, Application US/09526043
; Patent No. 6881555
; GENERAL INFORMATION:
; APPLICANT: Guo, Kun
; APPLICANT: Pagnoni, Marco
; APPLICANT: Clark, Kenneth
; APPLICANT: Ivaachenko, Yuri
; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
; FILE REFERENCE: A3278A-US
; CURRENT APPLICATION NUMBER: US/09/526.043
; CURRENT FILING DATE: 2000-03-14
; EARLIER APPLICATION NUMBER: 60/125,108
; EARLIER FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1570
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (126)..(1523)
US-09-526-043-1
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Pred. No.: 0 Length: 1570
Score: 451.00 Matches: 451
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 94.15% Indels: 0
DB: 3 Gaps: 0

US-09-869-079D-3 (1-479) x US-09-526-043-1 (1-1570)
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QY 21 AsnTrpArgProArgTyrPheLeuLeuLysThrAspGlySerPheIleGlyTyrLysGlu 40
DB 186 AACTGGAGGCCAAGATACCTCTTTTGAAGACAGATGCTCATTCATAGGATATAAAGAG 245
QY 41 LysProGlnAspValAspLeuProTyrProLeuAsnAsnPheSerValAlaLysCysGln 60
DB 246 AAACCTCAAGATGTGGATTTACCTTTATCCCTTCAACAACTTTTTCAGTGGCAAAATGCCAG 305
QY 61 LeuMetLysThrGluArgProLysProAsnThrPheIleIleArgCysLeuGlnTrpThr 80
DB 306 TTAATGAAAAACAGAACGACCAACCAACACATTTATTAATCAGATGTCTCCAGTGGACT 365
QY 81 ThrValIleGluArgThrPheHisValAspThrProGluGluArgGluGluTrpThrGlu 100
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Qy 121 ProThrSerGlnIleAspAsnIleGlyGluGluGluMetAspAlaSerThrThrHisHis 140
Db 486 CCAACTTCACAAATGATATATAGAGAGAGAGATGGATGGCTCTACAACCCATCAT 545
Qy 141 LysArgLysThrMetAsnAspPheAspTyrLeuLysLeuLeuGlyLysGlyThrPheGly 160
Db 546 AAAAGAAAGCAATGAATGATTTTGACTATTTGAACTACTAGTAAAGCACTTTTGGG 605
Qy 161 LysValIleLeuValArgGluLysAlaSerGlyLysTyrTyrAlaMetLysIleLeuLys 180
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Qy 241 ArgValPheSerGluAspArgThrArgPheTyrGlyAlaGluIleValSerAlaLeuAsp 260
Db 846 CGGGTGTCTCTGAGGACCGCACACGTTTCTATGGTGCAGAAATTTGCTCTGCTTGGAC 905
Qy 261 TyrLeuHisSerGlyLysIleValTyrArgAspLeuLysLeuGluAsnLeuMetLeuAsp 280
Db 906 TATCTCATTTCCGAAAGATGTGTACCGTGATCTCAAGTTGGAGAAATCTAATGCTGGAC 965
Qy 281 LysAspGlyHisIleLysIleThrAppPheGlyLeuCysLysGluGlyIleThrAspAla 300
Db 966 AAAGATGGCCACATAAAATATACAGATTTTGGACTTTTGCAAAAGAGGGATCACAGATGCA 1025
Qy 301 AlaThrMetLysThrPheCysGlyThrProGluTyrLeuAlaProGluValLeuGluAsp 320
Db 1026 GCCACCATGAAGACATTTCTGTGGCACTCCAGATATCTGGCACGAGAGGTGTAGAAGAT 1085
Qy 321 AsnAspTyrGlyArgAlaValAspTyrTrpGlyLeuGlyValValMetTyrGluMetMet 340
Db 1086 AATGACTATGGCGAGCAGTAGACTGGTGGGGCTAGGGGTGTGTCATGTATGAAATGATG 1145
Qy 341 CysGlyArgLeuProPheTyrAsnGlnAspHisGluLysLeuPheGluLeuLeuMet 360
Db 1146 TGTGGGAGGTTTACCTTTCTACAACAGGACCATGAGAACTTTTGTGAATTAATTAATG 1205
Qy 361 GluAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuSerGlyLeu 380
Db 1206 GAAGACATTAATTTCTCGAACACTCTCTTCAGATGCAAAATCATTTTCAGGGCTC 1265
Qy 381 LeuIleLysAspProAsnLysArgLeuGlyGlyProAspAspAlaLysGluIleMet 400
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Qy 401 ArgHisSerPhePheSerGlyValAsnTrpGlnAspValTyrAspLysLysLeuValPro 420
Db 1326 AGACACAGTTTCTTCTCTGGAGTAAACTGGCAAGATGTATATGATAAAAAGCTTGTACCT 1385
Qy 421 ProPheLysProGlnValThrSerGluThrAspThrArgTyrPheAspGluGluPheThr 440
Db 1386 CCTTTTAAACCTCAAGTAAACATCTGAGACAGATATAGATATTTTGTGAAGATTTTACA 1445
Qy 441 AlaGlnThrIleThrIleThrProProGluLys 451
Db 1446 GCTCAGACTATTACAAATAACACCCACCTGAAAAA 1478
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RESULT 3

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US-09-771-161A-66
; Sequence 66, Application US/09771161A
; Patent No. 6936450
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 66
; LENGTH: 2410
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-771-161A-66
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Score: 247.00 Matches: 247
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 51.57% Indels: 0
DB: 3 Gaps: 0
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US-09-869-079D-3 (1-479) x US-09-771-161A-66 (1-2410)

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Db 314 CTGTTTTTCCATTTGTTCGAGAGAGCGGGTCTCTCTGAGGACCGCACACGCTTTCTATGTT 373
Qy 253 AlaGluIleValSerAlaLeuAspTyrLeuHisSerGlyLysIleValTyrArgAspLeu 272
Db 374 GCAGAAATTTGTCTCTCCCTTGGACTATCTACATTCGCGAAGATTTGTATACCGGTGATCTC 433
Qy 273 LysLeuGluAsnLeuMetLeuAspLysAspGlyHisIleLysIleThrAspPheGlyLeu 292
Db 434 AAGTTGGAGAAATCTAATGCTGGCAAGATGGCCACATAAAAATTTACAGATTTTGGACTT 493
Qy 293 CysLysGluGlyIleThrAspAlaIleThrMetLysThrPheCysGlyThrProGluTyr 312
Db 494 TGCAAGAAGGGATCACAGATGCAGCCACCATGAGACATTTCTGTGGCAATAT 553
Qy 313 LeuAlaProGluValLeuGluAspAsnAspTyrGlyArgAlaValAspTyrTrpGlyLeu 332
Db 554 CTGGCACCAAGGTTGTAGAAATAATGACTATATGGCGGAGCAGTAGACTGGTGGGGCTA 613
Qy 333 GlyValValMetTyrGluMetMetCysGlyArgLeuProPheTyrAsnGlnAspHisGlu 352
Db 614 GGGTGTGTCATGTATGAAATGATGTGTGGAGGTACCTTTCTACAAACAGGACCATGAG 673
Qy 353 LysLeuPheGluLeuIleLeuMetGluAspIleLysPheProArgThrLeuSerSerAsp 372
Db 674 AAATTTTTTGAATTAATTAATGGAAGACATTTAAATTTCTCGAACACTCTCTTCAGAT 733
Qy 373 AlaLysSerLeuLeuSerGlyLeuLeuIleLysAspProAsnLysArgLeuGlyGly 392
Db 734 GCAAAATCATTTGCTTTCAGGGCTCTTGTATAAAGATCCAAATAAACCGCTTTGTGGAGGA 793
Qy 393 ProAspAspAlaLysGluIleMetArgHisSerPhePheSerGlyValAsnTrpGlnAsp 412
Db 794 CCAGATGATCAAAAGAAATTTATGAGACACAGATTTCTTCTCTGGAGTAAACTGGCAAGAT 853
Qy 413 ValTyrAspLysLysLeuValProPheLysProGlnValThrSerGluThrAspThr 432
```

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Db      854 GTATATGATAAAAAAGCTTGACTCTCTTTTAAACCTCAAGTAACATCTCTGAGACAGATACT 913
Qy      433 ArgTyrPheAspGluGluPheThrAlaGlnThrIleThrIleThrProProGluLysTyr 452
Db      914 AGATATTTTGATGAAGAATTTACAGCTCAGACTATTACAAATAACACCACCTGAAAAATAT 973
Qy      453 AspGluAspGlyMetAspCysMetAspAsnGluArgArgProHisPheProGlnPheSer 472
Db      974 GATGAGGATGGTATGGACTGCAATGGACAATGAGGCGCGCCGATTTCCCTCAATTTTCC 1033
Qy      473 TyrSerAlaSerGlyArgGlu 479
Db      1034 TACTCTGCAAGTGGACGAGAA 1054

RESULT 4
US-09-771-161A-65
; Sequence 65, Application US/09771161A
; Patent No. 6936450
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 65
; LENGTH: 968
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: -
; LOCATION: (1)..(968)
; OTHER INFORMATION: "n" can be any nucleotide 'a', 'c', 'g' or 't'
US-09-771-161A-65

Alignment Scores:
Pred. No.:      3,228-195      Length:      968
Score:          187.00      Matches:      187
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      39.04%      Indels:      0
DB:              3          Gaps:      0

US-09-869-079D-3 (1-479) x US-09-771-161A-65 (1-968)

Qy      1 MetSerAspValThrIleVallysGluGlyTyrValGlnLysArgGlyGluTyrIleLys 20
Db      154 ATGACCGATGTTACCATGTGAAAGAGGTTGGGTTCAAGAGGGGAGAAATATATAAAA 213
Qy      21 AsnTrpArgProArgTyrPheLeuLeuLysThrAspGlySerPheIleGlyTyrIysGlu 40
Db      214 AACTGGAGCCCAAGATACTCTCTTTTGAAGACAGATGGCTCATTCATAGGATATAAAG 273
Qy      41 LysProGlnAspValAspLeuProTyrProLeuAsnAsnPheSerValAlaLysCysGln 60
Db      274 AAACCTCAAGATGTGGATTTACCTTTATCCCTCAACAACATTTTTCAGTGCGCAAAATGCCAG 333
Qy      61 LeuMetLysThrGluArgProLysProAsnThrPheIleIleArgCysLeuGlnTrpThr 80
Db      334 TTAATGAACAACAGAACGACCAAGCCAAACACATTTATTAATCAGATGTCCTCAGTGGACT 393
Qy      81 ThrValIleGluArgThrPheHisValAspThrProGluGluArgGluGluTrpThrGlu 100
Db      394 ACTGTTATAGAGAGAACATTTTCATGTAGATATCTCCAGAGGAAAGGGAAGATGGACAGAA 453
Qy      101 AlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGluGluArgMetAsnCysSer 120
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Db      454 GCTATCCAGGCTGTAGCAGACAGACTGCAGAGGCAAGAGAGAGAGAAATGAATTTGTAGT 513
Qy      121 ProThrSerGlnIleAspAsnIleGlyGluGluMetAspAlaSerThrThrHisHis 140
Db      514 CCAACTTCACAATTTGATAATATAGGAGAGGAAGAGATGGATGCCTCTTACAAACCCATCAT 573
Qy      141 LysArgLysThrMetAsnAspPheAspTyrLeuLysLeuLeuGlyLysGlyThrPheGly 160
Db      574 AAAAGAAAAGACAAATGAATGATTTTGACTATTTTGAAACTACTAGGTAAAGGCCACTTTTGGG 633
Qy      161 LysValIleLeuValArgGluLysAlaSerGlyLysTyrTyrAlaMetLysIleLeuLys 180
Db      634 AAAGTTATTTGGTTTCGAGAGAAAGCAAGTGAAAAATACTATGCTATGAAGATTTCTGAAG 693
Qy      181 LysGluValIleIleAlaLys 187
Db      694 AAAGAAAGTCATTATTGCAAG 714

RESULT 5
US-09-474-922A-1
; Sequence 1, Application US/09474922A
; Patent No. 6187586
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; APPLICANT: Richard A. Roth
; TITLE OF INVENTION: ANTISENSE MODULATION OF Akt-3 EXPRESSION
; FILE REFERENCE: RTS-0036
; CURRENT APPLICATION NUMBER: US/09/474,922A
; CURRENT FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 1
; LENGTH: 403
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-474-922A-1

Alignment Scores:
Pred. No.:      1,89e-137      Length:      403
Score:          134.00      Matches:      134
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      27.97%      Indels:      0
DB:              3          Gaps:      0

US-09-869-079D-3 (1-479) x US-09-474-922A-1 (1-403)

Qy      7 VallysGluGlyTyrValGlnLysArgGlyGluTyrIleLysAsnTrpArgProArgTyr 26
Db      1 GTGAAAGAAAGGTTGGGTTCAAGAGAGGGGAGAAATATATAAAAACTGGAGGCCAAGATAC 60
Qy      27 PheLeuLeuLysThrAspGlySerPheIleGlyTyrLysGluLysProGlnAspValAsp 46
Db      61 TTCCTTTTGAAGACAGATGGCTCATTCATAGGATATAAAGAGAAACCTCAAGATGGAT 120
Qy      47 LeuProTyrProLeuAsnAsnPheSerValAlaLysCysGlnLeuMetLysThrGluArg 66
Db      121 TTACTTTATCCCTTCAACAACATTTTCAGTGGCAAAATGCCAGTTAATGAAAACAGAACGA 180
Qy      67 ProLysProAsnThrPheIleIleArgCysLeuGlnTrpThrThrValIleGluArgThr 86
Db      181 CCAAGGCCAAACACATTTATTAATCAGATGTCTCCAGTGGACTACTGTTTATAGAGAGAAC 240
Qy      87 PheHisValAspThrProGluGluArgGluGluTrpThrGluAlaIleGlnAlaValAla 106
Db      241 TTTTCATGTAGATATCTCCAGAGGAAAGGGAAGATGGACAGAGCTATATCCAGCTGTAGCA 300
Qy      107 AspArgLeuGlnArgGlnGluGluArgMetAsnCysSerProThrSerGlnIleAsp 126
Db      301 GACAGACTGACAGAGCAAGAGAGAGAGATGAATGATTTGTAGTCCCACTTCACAAATTGAT 360
Qy      127 AsnIleGlyGluGluMetAspAlaSerThrThrHisHis 140
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Qy	301	Ala	Thr	Met	I	Thr	Phe	Cys	Gly	Thr	Pro	Glu	Tyr	Leu	Ala	Pro	Glu	Val	Leu	Glu	Asp	321
Db	910	GCC	ACC	ATG	AGAC	CTTTT	GGG	CAC	ACCT	GAG	TAC	CTG	GGC	CGG	AGG	TCT	CGA	GAC				96
Qy	321	Asn	Asp	Tyr	Gly	Val	Gly	Leu	Gly	Val	Val	Met	Tyr	Glu	Met	Met						34

Db 970 AATGACTACGGCGGTGCAGCTGCTGGGGGCTGGCGGTGCATGTACGAGATGATG 1029
QY 341 CysGlyArgLeuProPheTyrAsnGlnAspHisGluLysLeuPheGluLeuIleLeuMet 360
Db 1030 TGGGGTGGCTGCCCTTCTACACAGGACCATGAGAACCTTTTGAGCTCATCTCATG 1089
QY 361 Glu 361
Db 1090 GAG 1092

RESULT 9

US-09-417-197-138
; Sequence 138, Application US/094117197
; Patent No. 6518021
; GENERAL INFORMATION:
; APPLICANT: Ole THASTRUP, et al.
; TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An I
; FILE OF INVENTION: On A Cellular Response
; FILE REFERENCE: 3759-0110P
; CURRENT APPLICATION NUMBER: US/09/417,197
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 138
; LENGTH: 2184
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EGFP-PKB fusion
; NAME/KEY: CDS
; LOCATION: (1)..(2181)
US-09-417-197-138

Alignment Scores:

Pred. No.:	1,27e-56	Length:	2184
Score:	61.00	Matches:	61
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	12.73%	Indels:	0
DB:	3	Gaps:	0

US-09-869-079D-3 (1-479) x US-09-417-197-138 (1-2184)

QY 301 AlathrMetLysThrPheCysGlyThrProGluTyrLeuAlaProGluValLeuGluAsp 320
Db 1651 GCCACATGAAGACCTTTTGGGCACACCTGAGTACCTGGCCCCCGAGGTGCTGGAGGAC 1710
QY 321 AsnAspTyrGlyArgAlaValAspTrpTrpGlyLeuGlyValValMetTyrGluMetMet 340
Db 1711 AATGACTACGGCGGTGCAGTGGCTGGTGGGGCTGGGGCTGGTGCATGTACGAGATGATG 1770
QY 341 CysGlyArgLeuProPheTyrAsnGlnAspHisGluLysLeuPheGluLeuIleLeuMet 360
Db 1771 TGGGGTGGCTGCCCTTCTACACAGGACCATGAGAACCTTTTGAGCTCATCTCATG 1830
QY 361 Glu 361
Db 1831 GAG 1833

RESULT 10

US-09-212-771-1
; Sequence 1, Application US/09212771
; Patent No. 5958773
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-1 EXPRESSION
; FILE REFERENCE: RTS-0034
; CURRENT APPLICATION NUMBER: US/09/212,771
; CURRENT FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1

; LENGTH: 2610
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (199)..(1641)
US-09-212-771-1

Alignment Scores:

Pred. No.:	1,52e-56	Length:	2610
Score:	61.00	Matches:	61
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	12.73%	Indels:	0
DB:	2	Gaps:	0

US-09-869-079D-3 (1-479) x US-09-212-771-1 (1-2610)

QY 301 AlathrMetLysThrPheCysGlyThrProGluTyrLeuAlaProGluValLeuGluAsp 320
Db 1108 GCCACATGAAGACCTTTTGGGCACACCTGAGTACCTGGCCCCCGAGGTGCTGGAGGAC 1167
QY 321 AsnAspTyrGlyArgAlaValAspTrpTrpGlyLeuGlyValValMetTyrGluMetMet 340
Db 1168 AATGACTACGGCGGTGCAGTGGCTGGTGGGGCTGGGGCTGGTGCATGTACGAGATGATG 1227
QY 341 CysGlyArgLeuProPheTyrAsnGlnAspHisGluLysLeuPheGluLeuIleLeuMet 360
Db 1228 TGGGGTGGCTGCCCTTCTACACAGGACCATGAGAACCTTTTGAGCTCATCTCATG 1287
QY 361 Glu 361
Db 1288 GAG 1290

RESULT 11

US-09-091-058-1
; Sequence 1, Application US/09091058
; Patent No. 6054285
; GENERAL INFORMATION:
; APPLICANT: Hemmings, Brian A.
; APPLICANT: Frech, Matthias
; TITLE OF INVENTION: Screening Method
; FILE REFERENCE: 4-20683/A/20684/PCT
; CURRENT APPLICATION NUMBER: US/09/091,058
; CURRENT FILING DATE: 1998-06-10
; EARLIER APPLICATION NUMBER: PCT/EP96/04814
; EARLIER FILING DATE: 1996-11-05
; EARLIER APPLICATION NUMBER: 9525703.6
; EARLIER FILING DATE: 1995-12-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2610
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (199)..(1641)
US-09-091-058-1

Alignment Scores:

Pred. No.:	1,52e-56	Length:	2610
Score:	61.00	Matches:	61
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	12.73%	Indels:	0
DB:	3	Gaps:	0

US-09-869-079D-3 (1-479) x US-09-091-058-1 (1-2610)

QY 301 AlathrMetLysThrPheCysGlyThrProGluTyrLeuAlaProGluValLeuGluAsp 320
Db 1108 GCCACATGAAGACCTTTTGGGCACACCTGAGTACCTGGCCCCCGAGGTGCTGGAGGAC 1167

QY 321 AenAspTyrGlyArgAlaValAspTrpTrpGlyLeuGlyValValMetTyrGluMetMet 340
|||
Db 1168 AATGACTACGGCGCGTGCAGTGGACTGGTGGGGCTGGGCGTGCATGTACGAGATGATG 1227
|||
QY 341 CysGlyArgLeuProPheTyrAsnGlnAspHisGluLysLeuPheGluLeuLeuMet 360
|||
Db 1228 TGGGTGCGCTGCCCTTCTACACGAGGACCATGAGAGCTTTTGGAGCTCATCCTCATG 1287
|||
QY 361 Glu 361
|||
Db 1288 GAG 1290

RESULT 12
US-09-023-655-1206
; Sequence 1206, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1206:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2610 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: G190827
US-09-023-655-1206

Alignment Scores:
Pred. No.: 1.52e-56 Length: 2610
Score: 61.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 12.73% Indels: 0
DB: 3 Gaps: 0

US-09-869-079D-3 (1-479) x US-09-023-655-1206 (1-2610)

QY 301 AlaThrMetLysThrPheCysGlyThrProGluTyrLeuAlaProGluValLeuGluAsp 320

Db 1108 GCCACCATGAAGACCTTTTGGCGCACACCTGAGTACCTGGCCCGGAGGTGCTGGAGGAC 1167
|||
QY 321 AenAspTyrGlyArgAlaValAspTrpTrpGlyLeuGlyValValMetTyrGluMetMet 340
|||
Db 1168 AATGACTACGGCGCGTGCAGTGGACTGGTGGGGCTGGGCGTGCATGTACGAGATGATG 1227
|||
QY 341 CysGlyArgLeuProPheTyrAsnGlnAspHisGluLysLeuPheGluLeuLeuMet 360
|||
Db 1228 TGGGTGCGCTGCCCTTCTACACGAGGACCATGAGAGCTTTTGGAGCTCATCCTCATG 1287
|||
QY 361 Glu 361
|||
Db 1288 GAG 1290

RESULT 13
US-09-590-740-1
; Sequence 1, Application US/09590740
; Patent No. 6689807
; GENERAL INFORMATION:
; APPLICANT: Kenneth Walsh
; APPLICANT: St. Elizabeth's Medical Center
; TITLE OF INVENTION: HMG CoA Reductase Inhibitors for
; TITLE OF INVENTION: Promoting Angiogenesis
; FILE REFERENCE: 49,784 (1417)
; CURRENT APPLICATION NUMBER: US/09/590,740
; CURRENT FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2610
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-590-740-1

Alignment Scores:
Pred. No.: 1.52e-56 Length: 2610
Score: 61.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 12.73% Indels: 0
DB: 3 Gaps: 0

US-09-869-079D-3 (1-479) x US-09-590-740-1 (1-2610)

QY 301 AlaThrMetLysThrPheCysGlyThrProGluTyrLeuAlaProGluValLeuGluAsp 320
|||
Db 1108 GCCACCATGAAGACCTTTTGGCGCACACCTGAGTACCTGGCCCGGAGGTGCTGGAGGAC 1167
|||
QY 321 AenAspTyrGlyArgAlaValAspTrpTrpGlyLeuGlyValValMetTyrGluMetMet 340
|||
Db 1168 AATGACTACGGCGCGTGCAGTGGACTGGTGGGGCTGGGCGTGCATGTACGAGATGATG 1227
|||
QY 341 CysGlyArgLeuProPheTyrAsnGlnAspHisGluLysLeuPheGluLeuLeuMet 360
|||
Db 1228 TGGGTGCGCTGCCCTTCTACACGAGGACCATGAGAGCTTTTGGAGCTCATCCTCATG 1287
|||
QY 361 Glu 361
|||
Db 1288 GAG 1290

RESULT 14
US-09-590-740-5
; Sequence 5, Application US/09590740
; Patent No. 6689807
; GENERAL INFORMATION:
; APPLICANT: Kenneth Walsh
; APPLICANT: St. Elizabeth's Medical Center
; TITLE OF INVENTION: HMG CoA Reductase Inhibitors for
; TITLE OF INVENTION: Promoting Angiogenesis
; FILE REFERENCE: 49,784 (1417)
; CURRENT APPLICATION NUMBER: US/09/590,740
; CURRENT FILING DATE: 2000-06-08

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; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 2626
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-590-740-5
```

```
Alignment Scores:
Pred. No.: 1.53e-56 Length: 2626
Score: 61.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 12.73% Indels: 0
DB: 3 Gaps: 0
```

US-09-869-079D-3 (1-479) x US-09-590-740-5 (1-2626)

```
QY 301 AlaThrMetLysThrPheCysGlyThrProGluTyrLeuAlaProGluValLeuGluAsp 320
Db 1193 GCCACTATGAAGACATTCTCGCGAAGCCGCGAGTACCTGGCCCTGAGGTGCTGGAGGAC 1252
QY 321 AsnAspTyrGlyArgAlaValAspTrpTrpGlyLeuGlyValValMetTyrGluMetMet 340
Db 1253 AACGACTACGCCGCGTGCAGTGGACTGGTGGGGCTGGGGCTGGTGCATGTATGAGATGATG 1312
QY 341 CysGlyArgLeuProPheTyrAsnGlnAspHisGluLysLeuPheGluLeuIleLeuMet 360
Db 1313 TGTGGCGCGCTGCCCTTCTTACACAGGACCAGAGAGCTGTTTCGAGCTGATCCTCATG 1372
QY 361 Glu 361
Db 1373 GAG 1375
```

RESULT 15

```
US-09-771-161A-64
; Sequence 64, Application US/09771161A
; Patent No. 6936450
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 64
; LENGTH: 765
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-771-161A-64
```

```
Alignment Scores:
Pred. No.: 1.09e-52 Length: 765
Score: 57.00 Matches: 57
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 11.90% Indels: 0
DB: 3 Gaps: 0
```

US-09-869-079D-3 (1-479) x US-09-771-161A-64 (1-765)

```
QY 1 MetSerAspValThrIleValLysGluGlyTrpValGlnLysArgGlyGluTyrIleLys 20
Db 154 ATGAGCGATGTTTACCATTTGTGAAGAGGTTGGTTTCAGAGAGGGGAGATATATATAA 213
QY 21 AsnTrpArgProArgTyrPheLeuLeuLysThrAspGlySerPheIleGlyTyrLysGlu 40
```

```
Db 214 AACTGGAGGCCCAAGATACTTCCCTTTTGAAGACAGATGGCTCATTCATAGGATATAAGAG 273
QY 41 LysProGlnAspValAspLeuProTyrProLeuAsnAsnPheSerValAla 57
Db 274 AAACCTCAAGATGTGGATTACCTTTATCCCTTCAACAACTTTTCAGTGGCA 324
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Search completed: December 24, 2005, 02:13:53
Job time : 258 secs